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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/020,743

DATE: 04/02/2001
TIME: 14:23:25

Input Set : A:\18547348.app
Output Set: N:\CRF3\04022001\I020743.raw

SEQUENCE LISTING
```
 4 (1) GENERAL INFORMATION:
 6      (i) APPLICANT: Mack, David H.
 8     (ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF
 9                              EXPRESSION COMPARISON
11    (iii) NUMBER OF SEQUENCES: 2          ,
13     (iv) CORRESPONDENCE ADDRESS:
14          (A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and
15                         Crew LLP
16          (B) STREET: Two Embarcadero Center, Eighth Floor
17          (C) CITY: San Francisco
18          (D) STATE: CA
19          (E) COUNTRY: USA
20          (F) ZIP: 94111-3834
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Floppy disk
24          (B) COMPUTER: IBM PC compatible
25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28     (vi) CURRENT APPLICATION DATA: `
C--> 29          (A) APPLICATION NUMBER: US/09/020,743
C--> 30          (B) FILING DATE: 09-Feb-1998
31          (C) CLASSIFICATION:
33   (viii) ATTORNEY/AGENT INFORMATION:
34          (A) NAME: Liebeschuetz, Joe
35          (B) REGISTRATION NUMBER: 37,505
36          (C) REFERENCE/DOCKET NUMBER: 018547034800US
38     (ix) TELECOMMUNICATION INFORMATION:
39          (A) TELEPHONE: (650) 326-2400
40          (B) TELEFAX: (650) 326-2422
43 (2) INFORMATION FOR SEQ ID NO: 1:
45      (i) SEQUENCE CHARACTERISTICS:
46          (A) LENGTH: 2691 base pairs
47          (B) TYPE: nucleic acid
48          (C) STRANDEDNESS: unknown
W--> 49          (D) TOPOLOGY: not relevant
51     (ii) MOLECULE TYPE: DNA (genomic)
53     (vi) ORIGINAL SOURCE:
54          (A) ORGANISM: Homo sapiens
58     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60 GGAGACAGAC AGACAGCTGG CAAGAGGCAG CCTGGGGGCC ACAGCTGCTT CAGCAGACCT      60
62 CATGGCTGAG TGAGCCTCCC CTGGGCCCAG CACCCCACCT CAGCATGGTC CAAGCCCATG     120
64 GGGGGCGCTC CAGAGCACAG CCGTTGACCT TGTCTTTGGG GGCAGCCATG ACCCAGCCTC     180
66 CGCCTGAAAA AACGCCAGCC AAGAAGCATG TGCGACTGCA GGAGAGGCGG GGCTCCAATG     240
68 TGGCTCTGAT GCTGGACGTT CGGTCCCTGG GGGCCGTAGA ACCCATCTGC TCTGTGAACA     300
70 CACCCCGGGA GGTCACCCTA CACTTTCTGC GCACTGCTGG ACACCCCCTT ACCCGCTGGG     360
72 CCCTTCAGCG CCAGCCACCC AGCCCCAAGC AACTGGAAGA AGAATTCTTG AAGATCCCTT     420
```

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```
 74 CAAACTTTGT CAGCCCCGAA GACCTGGACA TCCCTGGCCA CGCCTCCAAG GACCGATACA      480
 76 AGACCATCTT GCCAAATCCC CAGAGCCGTG TCTGTCTAGG CCGGGCACAG AGCCAGGAGG      540
 78 ACGGAGATTA CATCAATGCC AACTACATCC GAGGCTATGA CGGGAAGGAG AAGGTCTACA      600
 80 TTGCCACCCA GGGCCCCATG CCCAACACTG TGTCGGACTT CTGGGAGATG GTGTGGCAAG      660
 82 AGGAAGTGTC CCTCATTGTC ATGCTCACTC AGCTCCGAGA GGGCAAGGAG AAATGTGTCC      720
 84 ACTACTGGCC CACAGAAGAG GAAACCTATG GACCCTTCCA GATCCGCATC CAGGACATGA      780
 86 AAGAGTGCCC AGAATACACT GTGCGGCAGC TCACCATCCA GTACCAGGAA GAGCGCCGGT      840
 88 CAGTAAAGCA CATCCTCTTT TCGGCCTGGC CAGACCATCA GACACCAGAA TCAGCTGGGC      900
 90 CCCTGCTGCG CCTAGTGGCA GAGGTGGAGG AGAGCCCGGA GACAGCCGCC CACCCCGGGC      960
 92 CTATCGTAGT CCACTGCAGT GCAGGGATTG GCCGGACGGG CTGCTTCATC GCCACGCGAA     1020
 94 TTGGCTGTCA ACAGCTGAAA GCCCGAGGAG AAGTGGACAT TCTGGGTATT GTGTGCCAAC     1080
 96 TGCGGCTAGA CAGAGGGGGG ATGATCCAGA CGGACGAGCA GTACCAGTTC CTGCACCACA     1140
 98 CTTTGGCCCT GTATGCAGGC CAGCTGCCTG AGGAACCCAG CCCCTGACCC CTGCCACCCT     1200
100 CCGGTGGCCC AGGTGCCTAC CTCCCTCAAG CCTGGGAAGT CACAGGAAGC AGCAGCAGTA     1260
102 AGGACAAGGG GCCGGATTCC AGGTCTTCAA CACTGGCCAC TCCTCTGCTT CCTCTGTTGG     1320
104 CCCCAGATGG ACAGTAAGGG GAACCTCCAA TGTCTCTCTG AACTTAAAGA CAGGAGCTGG     1380
106 CATTTATGAC AGACAAAGAA AGAAGCCCAG GTGTCCTGGT GTTCTCTGAG ACACTCTTTG     1440
108 TGAGCTTCAG TTTCCTGTTC TATAACATGA ACATAAGTGC TTAGCTGCCA TGAGGGAAAA     1500
110 GTAATGAGAG AAGTTTCTAG AAGCCACTCC AGCCACTCCT TCCTGGGGCT GACAAAAGGG     1560
112 TGATTCCAAG ATCATCCTTC ACCCGAGGTC CTGCCCAAGC ACAGGCCAGA TGCAAGAATG     1620
114 GGGAAAAGTC TGGTCCTGAT CTCCAAGTCT CAACATCCTA TCAGTGACTC TGCTCCCTGA     1680
116 CCACACATCG GAAGGGCTGG ATGACCCCAA TCAAAAGAAA GAACAAGGAC TCTGGTTACC     1740
118 CTTGCCCTCC ACCCATGTGT CATAAGAGTA GGCTACAGAG GTGACCAGGC CTGGCAGTTG     1800
120 AAATCTCTGG AAGAGGGAAC ATGTGGGGAC TACTCAGAGG CAAAGAGGAG CTGCTCCTGC     1860
122 CTCCATGGTT GCTGGCCACT CCCACCAACT ACTCTTAGGG AGGCTAAGCA GTCTCTGTTT     1920
124 TGCTTCCATG GCTCAAATAA TACCCTGGGT ATGCAGGACC CACTATACCT TGCATTTGCT     1980
126 GGTACACCTA GAGAGCTTGG CTGTTTCCAA AAACAATCAG GGTCATAACC ATCCATGCAG     2040
128 ACATGGAGGC TCGGCTGAAC CAGGACTCCT CACTGTCTAC CTGAGAGAAT GAGCACCCCT     2100
130 CATCCATCTC AGCATCAACA CAATTTCCAG GGGACCTCAG GTCTACCTCA GGACTGAACG     2160
132 CCACACCTCA GGATTCCTCC TCCTTGAATC TGAGACTGGC TGCCCATTCT GAGATGGGGA     2220
134 TGAAGGTAAG ATGCCGCATC ACCAGGCACG CCGCCCCTGA CAGCTGCCTT GATACCAGCT     2280
136 CTCTGTGGAA ACCCCGAGG_AGTTGGATCT GGAGAACAGC TGGGCCTCCT CACTCAGGAC     2340
138 TTCTCTCCTG AAGAACACGC AGTGCTAAAA CTGAGGATGA TTTCCCTAAT GCTTCTGCTT     2400
140 GGCCTTATGG AGGAGCTGCT CCTTCCTTAC AGCCTTGGGG ATGGACTTGC CCACACCTCC     2460
142 ACCTCCCCTG AGCCCTGTGA GAGGCACGAC TGTCTATGCC AATGAGGCTC GGTGGGGGGC     2520
144 TCTCAAGTGC CTGATCCTGC CCTGGGCTCA GAGCCAGCCC AGAGGGAAGC AACTGCACAG     2580
146 CCCCACAGGC CCTCCCTGGC ACTGTCCCCC CAACCCCATC TCAGAGCTCA GAGGGTACAA     2640
148 GCTCCAGAAC AGTAACCAAG TGGGAAAATA AAGACTTCTT GGATGACTGA C               2691
150 (2) INFORMATION FOR SEQ ID NO: 2:
152      (i) SEQUENCE CHARACTERISTICS:
153          (A) LENGTH: 360 amino acids
154          (B) TYPE: amino acid
155          (C) STRANDEDNESS: not relevant
156          (D) TOPOLOGY: not relevant
158      (ii) MOLECULE TYPE: protein
160      (vi) ORIGINAL SOURCE:
161          (A) ORGANISM: Homo sapiens
165      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
167      Met Val Gln Ala His Gly Gly Arg Ser Arg Ala Gln Pro Leu Thr Leu
```

W--> 156

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```
168    1               5                    10                   15
170    Ser Leu Gly Ala Ala Met Thr Gln Pro Pro Pro Glu Lys Thr Pro Ala
171            20                  25                  30
173    Lys Lys His Val Arg Leu Gln Glu Arg Arg Gly Ser Asn Val Ala Leu
174            35                  40                  45
176    Met Leu Asp Val Arg Ser Leu Gly Ala Val Glu Pro Ile Cys Ser Val
177            50                  55                  60
179    Asn Thr Pro Arg Glu Val Thr Leu His Phe Leu Arg Thr Ala Gly His
180    65                  70                  75                  80
182    Pro Leu Thr Arg Trp Ala Leu Gln Arg Gln Pro Pro Ser Pro Lys Gln
183            85                  90                  95
185    Leu Glu Glu Glu Phe Leu Lys Ile Pro Ser Asn Phe Val Ser Pro Glu
186            100                 105                 110
188    Asp Leu Asp Ile Pro Gly His Ala Ser Lys Asp Arg Tyr Lys Thr Ile
189            115                 120                 125
191    Leu Pro Asn Pro Gln Ser Arg Val Cys Leu Gly Arg Ala Gln Ser Gln
192            130                 135                 140
194    Glu Asp Gly Asp Tyr Ile Asn Ala Asn Tyr Ile Arg Gly Tyr Asp Gly
195    145                 150                 155                 160
197    Lys Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Met Pro Asn Thr Val
198            165                 170                 175
200    Ser Asp Phe Trp Glu Met Val Trp Gln Glu Glu Val Ser Leu Ile Val
201            180                 185                 190
203    Met Leu Thr Gln Leu Arg Glu Gly Lys Glu Lys Cys Val His Tyr Trp
204            195                 200                 205
206    Pro Thr Glu Glu Glu Thr Tyr Gly Pro Phe Gln Ile Arg Ile Gln Asp
207            210                 215                 220
209    Met Lys Glu Cys Pro Glu Tyr Thr Val Arg Gln Leu Thr Ile Gln Tyr
210    225                 230                 235                 240
212    Gln Glu Glu Arg Arg Ser Val Lys His Ile Leu Phe Ser Ala Trp Pro
213            245                 250                 255
215    Asp His Gln Thr Pro Glu Ser Ala Gly Pro Leu Leu Arg Leu Val Ala
216            260                 265                 270
218    Glu Val Glu Glu Ser Pro Glu Thr Ala Ala His Pro Gly Pro Ile Val
219            275                 280                 285
221    Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Cys Phe Ile Ala Thr
222            290                 295                 300
224    Arg Ile Gly Cys Gln Gln Leu Lys Ala Arg Gly Glu Val Asp Ile Leu
225    305                 310                 315                 320
227    Gly Ile Val Cys Gln Leu Arg Leu Asp Arg Gly Gly Met Ile Gln Thr
228            325                 330                 335
230    Asp Glu Gln Tyr Gln Phe Leu His His Thr Leu Ala Leu Tyr Ala Gly
231            340                 345                 350
233    Gln Leu Pro Glu Glu Pro Ser Pro
234            355                 360
```

VERIFICATION SUMMARY   DATE: 04/02/2001
PATENT APPLICATION: US/09/020,743   TIME: 14:23:26

Input Set : **A:\18547348.app**
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```
L:29  M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30  M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:49  M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
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